LISTING OF CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application:

1-37. **(Canceled).**

38. **(Currently amended)** A method to identify a compound that modulates a direct interaction between one or more subunits of a SWI/SNF chromatin remodeling complex and a nucleic acid regulatory protein DNA binding domain peptide, the method comprising:

a) providing one or more subunits of a SWI/SNF chromatin remodeling complex and a nucleic acid regulatory protein zinc finger DNA binding domain peptide under conditions that permit the direct interaction of the one or more subunits of the chromatin remodeling complex and the zinc finger DNA binding domain peptide ~~to form a multi-subunit protein complex~~;

b) contacting ~~the multi-subunit protein complex~~ with a test compound the zinc finger DNA binding domain peptide in direct interaction with the one or more subunits of a SWI/SNF chromatin remodeling complex; and

c) determining whether there is an increase or decrease in the direct interaction between the one or more subunits of the chromatin remodeling complex and the zinc finger DNA binding domain peptide, wherein an increase or decrease identifies the test compound as a compound that modulates the direct interaction between the one or more subunits of the chromatin remodeling complex and the zinc finger DNA binding domain peptide.

39. **(Canceled).**

40. **(Previously presented)** The method of claim 38, wherein the nucleic acid regulatory protein is a transcription factor.

41-53. **(Canceled).**

54. **(Previously presented)** The method of claim 38, wherein the nucleic acid regulatory protein is selected from the group consisting of GATA-1, Spl, EKLF, FKLF, BKLF, GKLF, LKLF, Wilm's tumor suppressor protein (WT1), BRCA1, BRCA2, KRAB, BTB/POZ, Zif268, GLI, Xfin, a BTB/POZ domain containing zinc finger protein, PLZF (promyelocytic leukemia zinc finger), and a nuclear hormone receptor.

55. **(Previously presented)** The method of claim 41, wherein the zinc finger domain is from a nuclear hormone receptor.

56. **(Previously presented)** The method of claim 55, wherein the nuclear hormone receptor is selected from the group consisting of an androgen, estrogen, thyroid, progesterone, and glucocorticoid receptor.

57-62. **(Canceled).**

63. **(Currently amended)** A method to identify a compound that modulates chromatin remodeling of a specific DNA sequence within chromatin comprising:

a) providing chromatin assembled DNA containing a specific DNA sequence, which specific DNA sequence comprises a binding site for a DNA binding domain peptide of a nucleic acid regulatory protein;

b) contacting the chromatin assembled DNA with one or more subunits of an SWI/SNF chromatin remodeling complex, and the DNA binding domain peptide of the nucleic acid regulatory protein; and

c) determining the level of chromatin remodeling in the presence and absence of ~~the~~a test compound; wherein a difference in the level of chromatin remodeling in the presence and absence of the test compound identifies the test compound as a compound that modulates chromatin remodeling of the specific DNA sequence within chromatin.

64. **(Previously presented)** The method of claim 63, wherein the specific DNA sequence is an individual gene or portion thereof, a regulatory region or a chromosomal region.

65. **(Canceled).**

66. **(Previously presented)** The method of claim 63, wherein the nucleic acid regulatory protein is a transcription factor.

67. **(Canceled).**

68. **(Previously presented)** The method of claim 63, wherein the DNA binding domain is a zinc-finger domain, a helix-turn-helix domain, or a helix loop helix domain containing a leucine zipper motif.

69-71. **(Canceled).**

72. **(Previously presented)** The method of claim 63, wherein the SWI/SNF complex is E-RC1.

73. **(Previously presented)** The method of claim 63, wherein the SWI/SNF complex is BRM.

74. **(Previously presented)** The method of claim 63, wherein the chromatin remodeling complex comprises BRG1.

75. **(Previously presented)** The method of claim 63, wherein the chromatin remodeling complex comprises BAF 155.

76. **(Previously presented)** The method of claim 63, wherein the chromatin remodeling complex comprises BAF 170.

77. **(Previously presented)** The method of claim 63, wherein the chromatin remodeling complex comprises BRG1 and BAF 155.

78. **(Canceled).**

79. **(Previously presented)** The method of claim 63, wherein the one or more subunits of a chromatin remodeling complex are selected from the group consisting of BRG1, BRM, BAF 155, BAF 170, INil, BAF 60, BAF 47 and BAF 57.

80. **(Previously presented)** The method of claim 63, wherein the nucleic acid regulatory protein is selected from the group consisting of GATA-1, Spl, EKLF, FKLF, BKLF, GKLF, LKLF, Wilm's tumor suppressor protein (WT1), BRCAI, BRCA2, KRAB, BTB/POZ, Zif268, GLI, Xfin, a BTB/POZ domain containing zinc finger protein, PLZF (promyelocytic leukemia zinc finger), and a nuclear hormone receptor.

81. **(Previously presented)** The method of claim 63, wherein the DNA binding domain is from a nuclear hormone receptor.

82. **(Previously presented)** The method of claim 81, wherein the nuclear hormone receptor is selected from the group consisting of an androgen, estrogen, thyroid, progesterone, and glucocorticoid receptor.

83. **(Previously presented)** The method of claim 63, wherein the DNA binding domain peptide binds to a promoter, an enhancer, an insulator, a silencer, or locus of control regions (LCRs).

84. **(Previously presented)** The method of claim 63, wherein the test compound is a small molecule.

85. **(Previously presented)** The method of claim 63, wherein the test compound is a peptide.

86. **(Canceled).**

87. **(Previously presented)** The method of claim 63, further comprising determining whether the compound modulates the expression of a chromatin-assembled DNA sequence comprising the specific DNA sequence.

88. **(Previously presented)** The method of claim 63, wherein the amount of chromatin remodeling is determined by assaying for DNAse hypersensitive sites within the specific DNA sequence.

89-99. **(Canceled).**